

10/540546

09598

JC17 Rec'd PCT/PTO 24 JUN 2005

SEQUENCE LISTING

<110> Fujisawa Pharmaceutical Co., Ltd.
 <120> New methods for selecting an immunosuppressive agent
 <130> 09598
 <150> JP2002-378800
 <151> 2002-12-27
 <160> 86
 <170> PatentIn version 3.1
 <210> 1
 <211> 3255
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1).. (3255)
 <223> human histone deacetylase-4 (HDAC4) gene
 <400> 1
 atg agc tcc caa agc cat cca gat gga ctt tct ggc cga gac cag cca 48
 Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
 1 5 10 15
 gtg gag ctg ctg aat cct gcc cgc gtg aac cac atg ccc agc acg gtg 96
 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
 20 25 30
 gat gtg gcc acg ggc ctg cct ctg caa gtg gcc ccc tcg gca gtg ccc 144
 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
 35 40 45
 atg gac ctg cgc ctg gac cac cag ttc tca ctg cct gtg gca gag ccg 192
 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
 50 55 60
 gcc ctg cgg gag cag cag ctg cag cag gag ctc ctg gcg ctc aag cag 240
 Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Ala Leu Lys Gln
 65 70 75 80
 aag cag cag atc cag agg cag atc ctc atc gct gag ttc cag agg cag 288
 Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
 85 90 95
 cac gag cag ctc tcc cgg cag cac gag gcg cag ctc cac gag cac atc 336
 His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
 100 105 110
 aag caa caa cag gag atg ctg gcc atg aag cac cag cag gag ctg ctg 384
 Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
 115 120 125
 gaa cac cag cgg aag ctg gag agg cac cgc cag gag cag gag ctg gag 432
 Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu
 130 135 140
 aag cag cac cgg gag cag aag ctg cag cag ctc aag aac aag gag aag 480
 Lys Gln His Arg Glu Gln Lys Leu Gln Gln Lys Lys Asn Lys Glu Lys
 145 150 155 160
 ggc aaa gag agt gcc gtg gcc agc aca gaa gtg aag atg aag tta caa 528
 Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln
 165 170 175
 gaa ttt gtc ctc aat aaa aag aag gcg ctg gcc cac cgg aat ctg aac 576
 Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn
 180 185 190
 cac tgc att tcc agc gac cct cgc tac tgg tac ggg aaa acg cag cac 624

(1)

09598

His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His	
195 200 205	
agt tcc ctt gac cag agt tct cca ccc cag agc gga gtg tgg acc tcc	672
Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser	
210 215 220	
tat aac cac ccg gtc ctg gga atg tac gac gcc aaa gat gac ttc cct	720
Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro	
225 230 235	
ctt agg aaa aca gct tct gaa ccg aat ctg aaa tta cgg tcc agg cta	768
Leu Arg Lys Thr Val Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu	
245 250 255	
aag cag aaa gtg gcc gaa aga ccg agc agc ccc ctg tta cgc agg aaa	816
Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys	
260 265 270	
gac ggg cca gtg gtc act gct cta aaa aag cgt ccg ttg gat gtc aca	864
Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr	
275 280 285	
gac tcc gcg tgc agc agc gcc cca ggc tcc gga ccc agc tca ccc aac	912
Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn	
290 295 300	
aac agc tcc ggg agc gtc agc gcg gag aac ggt atc gcg ccc gcc gtc	960
Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val	
305 310 315 320	
ccc agc atc ccg gcg gag acg agt ttg gcg cac aga ctt gtg gca cga	1008
Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg	
325 330 335	
gaa ggc tgg gcc gct cca ctt ccc ctg tac aca tgg cca tcc ttg ccc	1056
Glu Gly Ser Ala Ala Pro Leu Pro Tyr Thr Ser Pro Ser Leu Pro	
340 345 350	
aac atc acg ctg ggc ctg cct gcc acc ggc ccc tct gcg ggc acg gcg	1104
Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala	
355 360 365	
ggc cag cag gac acc gag aga ctg acc ctt ccc gcc ctg cag cag agg	1152
Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg	
370 375 380	
ctc tcc ctt ttc ccc ggc acc cac ctg act ccc tac ctg agc acc tgg	1200
Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser	
385 390 395 400	
ccc ttg gag ccg gac gga ggg gca gcg cac agc cct ctt ctg cag cac	1248
Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His	
405 410 415	
atg gtc tta ctg gag cag cca ccg gca caa gca ccc ctg gtc aca ggc	1296
Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly	
420 425 430	
ctg gga gca ctg ccc ctg cac gca cag tcc ttg gtt ggt gca gac ccg	1344
Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg	
435 440 445	
gtg tcc ccc tcc atc cac aag ctg ccg cag cac ccg cca ctg ggg ccg	1392
Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg	
450 455 460	
acc cag tgg gcc ccg ctg ccc cag aac gcc cag gct ctg cag cac ctg	1440
Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu	
465 470 475 480	
gtc atc cag cag cag cat cag cag ttt ctg gag aaa cac aag cag cag	1488
Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln	
485 490 495	

09598

ttc cag cag cag caa ctg cag atg aac aag atc atc ccc aag cca agc Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser 500 505 510	1536
gag cca gcc cgg cag ccg gag agc cac ccg gag gag acg gag gag gag Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu 515 520 525	1584
ctc cgt gag cac cag gct ctg ctg gac gag ccc tac ctg gac cgg ctg Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu 530 535 540	1632
ccg ggg cag aag gag gcg cac gca cag gcc ggc gtg cag gtg aag cag Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln 545 550 555 560	1680
gag ccc att gag agc gat gag gaa gag gca gag ccc cca cgg gag gtg Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val 565 570 575	1728
gag ccg ggc cag cgc cag ccc agt gag cag gag ctg ctc ttc aga cag Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln 580 585 590	1776
caa gcc ctc ctg ctg gag cag cag cgg atc cac cag ctg agg aac tac Gln Ala Leu Leu Leu Glu Gln Arg Ile His Gln Leu Arg Asn Tyr 595 600 605	1824
cag gcg tcc atg gag gcc gcc ggc atc ccc gtg tcc ttc ggc ggc cac Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His 610 615 620	1872
agg cct ctg tcc cgg gcg cag tcc tca ccc gcg tct gcc acc ttc ccc Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro 625 630 635 640	1920
gtg tct gtg cag gag ccc ccc acc aag ccg agg ttc acg aca ggc ctc Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu 645 650 655	1968
gtg tat gac acg ctg atg ctg aag cac cag tgc acc tgc ggg agt agc Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser 660 665 670	2016
agc agc cac ccc gag cac gcc ggg agg atc cag agc atc tgg tcc cgc Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg 675 680 685	2064
ctg cag gag acg ggc ctc cgg ggc aaa tgc gag tgc atc cgc gga cgc Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg 690 695 700	2112
aag gcc acc ctg gag gag cta cag acg gtg cac tog gaa gcc cac acc Lys Ala Thr Leu Glu Leu Gln Thr Val His Ser Glu Ala His Thr 705 710 715 720	2160
ctc ctg tat ggc acg aac ccc ctc aac cgg cag aaa ctg gac agt aag Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys 725 730 735	2208
aaa ctt cta ggc tog ctc gcc tcc gtg ttc gtc cgg ctc cct tgc ggt Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly 740 745 750	2256
ggt gtt ggg gtg gac agt gac acc ata tgg aac gag gtg cac tog gcg Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala 755 760 765	2304
ggg gca gcc cgc ctg gct gtg ggc tgc gtg gta gag ctg gtc ttc aag Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys 770 775 780	2352
gtg gcc aca ggg gag ctg aag aat ggc ttt gct gtg gtc cgc ccc cct Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro 785 790 795 800	2400

09598

gga cac cat gcg gag gag agc acg ccc atg ggc ttt tgc tac ttc aac Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn 805 810 815	2448
tcc gtg gcc gtg gca gcc aag ctt ctg cag cag agg ttg agc gtg agc Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser 820 825 830	2496
aag atc ctc atc gtg gac tgg gac gtg cac cat gga aac ggg acc cag Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln 835 840 845	2544
cag gct ttc tac agc gac cct agc gtc ctg tac atg tcc ctc cac cgc Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg 850 855 860	2592
tac gac gat ggg aac ttc ttc cca ggc agc ggg gct cct gat gag gtg Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val 865 870 875 880	2640
ggc aca ggg ccc ggc gtg ggt ttc aac gtc aac atg gct ttc acc ggc Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly 885 890 895	2688
ggc ctg gac ccc ccc atg gga gac gct gag tac ttg gcg gcc ttc aga Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg 900 905 910	2736
acg gtg gtc atg ccg atc gcc agc gag ttt gcc ccg gat gtg gtg ctg Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu 915 920 925	2784
gtg tca tca ggc ttc gat gcc gtg gag ggc cac ccc acc cct ctt ggg Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly 930 935 940	2832
ggc tac aac ctc tcc gcc aga tgc ttc ggg tac ctg acg aag cag ctg Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu 945 950 955 960	2880
atg ggc ctg gct ggc ggc cgg att gtc ctg gcc ctc gag gga ggc cac Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His 965 970 975	2928
gac ctg acc gcc att tgc gac gcc tgc gaa gca tgt gtt tct gcc ttg Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu 980 985 990	2976
ctg gga aac gag ctt gat cct ctc cca gaa aag gtt tta cag caa aga Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg 995 1000 1005	3024
ccc aat gca aac gct gtc cgt tcc atg gag aaa gtc atg gag atc cac Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His 1010 1015 1020	3072
agc aag tac tgg cgc tgc ctg cag cgc aca acc tcc aca gcg ggg cgt Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg 1025 1030 1035 1040	3120
tct ctg atc gag gct cag act tgc gag aac gaa gaa gcc gag acg gtc Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val 1045 1050 1055	3168
acc gcc atg gcc tgc ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg 1060 1065 1070	3216
cca gat gag gag ccc atg gaa gag gag ccg ccc ctg tag Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu 1075 1080	3255

<211> 1084
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
 1 5 10 15
 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
 20 25 30
 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
 35 40 45
 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
 50 55 60
 Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
 65 70 75 80
 Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
 85 90 95
 His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
 100 105 110
 Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
 115 120 125
 Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu
 130 135 140
 Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys
 145 150 155 160
 Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln
 165 170 175
 Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn
 180 185 190
 His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His
 195 200 205
 Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser
 210 215 220
 Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro
 225 230 235 240
 Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu
 245 250 255
 Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
 260 265 270
 Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr
 275 280 285
 Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn
 290 295 300
 Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val
 305 310 315 320
 Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg
 325 330 335
 Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro
 340 345 350
 Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala
 355 360 365
 Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg

09598

370

375

380

Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser
 385 390 395 400
 Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His
 405 410 415
 Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly
 420 425 430
 Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg
 435 440 445
 Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg
 450 455 460
 Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu
 465 470 475 480
 Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln
 485 490 495
 Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser
 500 505 510
 Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu
 515 520 525
 Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu
 530 535 540
 Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln
 545 550 555 560
 Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val
 565 570 575
 Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln
 580 585 590
 Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr
 595 600 605
 Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His
 610 615 620
 Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro
 625 630 635 640
 Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu
 645 650 655
 Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser
 660 665 670
 Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg
 675 680 685
 Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg
 690 695 700
 Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr
 705 710 715 720
 Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys
 725 730 735
 Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly
 740 745 750
 Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala
 755 760 765
 Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys

09598

770

775

780

Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro
 785 790 795 800
 Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn
 805 810 815
 Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser
 820 825 830
 Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln
 835 840 845
 Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg
 850 855 860
 Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val
 865 870 875 880
 Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly
 885 890 895
 Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg
 900 905 910
 Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu
 915 920 925
 Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly
 930 935 940
 Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu
 945 950 955 960
 Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His
 965 970 975
 Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu
 980 985 990
 Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
 995 1000 1005
 Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
 1010 1015 1020
 Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
 1025 1030 1035 1040
 Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
 1045 1050 1055
 Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg
 1060 1065 1070
 Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu
 1075 1080

<210> 3

<211> 3255

<212> DNA

<213> Artificial

<220>

<221> CDS

<222> (1)..(3255)

<223> Dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

<400> 3

atg agc tcc caa agc cat cca gat gga ctt tct ggc cga gac cag cca
 Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
 1 5 10 15

48

(7)

09598

gtg gag ctg ctg aat cct gcc cgc gtg aac cac atg ccc agc acg gtg Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val 20 25 30	96
gat gtg gcc acg gcg ctg cct ctg caa gtg gcc ccc tcg gca gtg ccc Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro 35 40 45	144
atg gac ctg cgc ctg gac cac cag ttc tca ctg cct gtg gca gag ccg Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro 50 55 60	192
gcc ctg cgg gag cag cag ctg cag cag gag ctc ctg gcg ctc aag cag Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln 65 70 75 80	240
aag cag cag atc cag agg cag atc ctc atc gct gag ttc cag agg cag Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln 85 90 95	288
cac gag cag ctc tcc cgg cag cac gag gcg cag ctc cac gag cac atc His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile 100 105 110	336
aag caa caa cag gag atg ctg gcc atg aag cac cag cag gag ctg ctg Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu 115 120 125	384
gaa cac cag cgg aag ctg gag agg cac cgc cag gag cag gag ctg gag Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu 130 135 140	432
aag cag cac cgg gag cag aag ctg cag cag ctc aag aac aag gag aag Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys 145 150 155 160	480
ggc aaa gag agt gcc gtg gcc agc aca gaa gtg aag atg aag tta caa Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln 165 170 175	528
gaa ttt gtc ctc aat aaa aag aag gcg ctg gcc cac cgg aat ctg aac Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn 180 185 190	576
cac tgc att tcc agc gac cct cgc tac tgg tac ggg aaa acg cag cac His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His 195 200 205	624
agt tcc ctt gac cag agt tct cca ccc cag agc gga gtg tcg acc tcc Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser 210 215 220	672
tat aac cac ccg gtc ctg gga atg tac gac gcc aaa gat gac ttc cct Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro 225 230 235 240	720
ctt agg aaa aca gct tct gaa ccg aat ctg aaa tta cgg tcc agg cta Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu 245 250 255	768
aag cag aaa gtg gcc gaa aga cgg agc agc ccc ctg tta cgc agg aaa Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys 260 265 270	816
gac ggg cca gtg gtc act gct cta aaa aag cgt ccg ttg gat gtc aca Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr 275 280 285	864
gac tcc gcg tgc agc agc gcc cca ggc tcc gga ccc agc tca ccc aac Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn 290 295 300	912
aac agc tcc ggg agc gtc agc gcg gag aac ggt atc gcg ccc gcc gtc Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val 305 310 315 320 325 330 335 340	960

305	310	315	09598	320	
ccc agc atc ccg gcg gag acg agt ttg gcg cac aga ctt gtg gca cga Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg 325 330 335					1008
gaa ggc tcg gcc gct cca ctt ccc ctc tac aca tcg cca tcc ttg ccc Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro 340 345 350					1056
aac atc acg ctg ggc ctg cct gcc acc ggc ccc tot gcg ggc acg gcg Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala 355 360 365					1104
ggc cag cag gac acc gag aga ctc acc ctt ccc gcc ctc cag cag agg Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg 370 375 380					1152
ctc tcc ctt ttc ccc ggc acc cac ctc act ccc tac ctg agc acc tcg Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser 385 390 395 400					1200
ccc ttg gag cgg gac gga ggg gca gcg cac agc cct ctt ctg cag cac Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His 405 410 415					1248
atg gtc tta ctg gag cag cca ccg gca caa gca ccc ctc gtc aca ggc Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly 420 425 430					1296
ctg gga gca ctg ccc ctc cac gca cag tcc ttg gtt ggt gca gac cgg Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg 435 440 445					1344
gtg tcc ccc tcc atc cac aag ctg cgg cag cac cgc cca ctg ggg cgg Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg 450 455 460					1392
acc cag tcg gcc ccg ctg ccc cag aac gcc cag gct ctg cag cac ctg Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu 465 470 475 480					1440
gtc atc cag cag cag cat cag cag ttt ctg gag aaa cac aag cag cag Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln 485 490 495					1488
ttc cag cag cag caa ctg cag atg aac aag atc atc ccc aag cca agc Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser 500 505 510					1536
gag cca gcc cgg cag ccg gag agc cac ccg gag gag acg gag gag gag Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu 515 520 525					1584
ctc cgt gag cac cag gct ctg ctg gac gag ccc tac ctg gac cgg ctg Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu 530 535 540					1632
ccg ggg cag aag gag gcg cac gca cag gcc ggc gtg cag gtg aag cag Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln 545 550 555 560					1680
gag ccc att gag agc gat gag gaa gag gca gag ccc cca cgg gag gtg Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val 565 570 575					1728
gag ccg ggc cag cgc cag ccc agt gag cag gag ctg ctc ttc aga cag Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln 580 585 590					1776
caa gcc ctc ctg ctg gag cag cag cgg atc cac cag ctg agg aac tac Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr 595 600 605					1824
cag gcg tcc atg gag gcc gcc ggc atc ccc gtg tcc ttc ggc ggc cac					1872

09598

Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His	
610 615 620	
agg cct ctg tcc cgg gcg cag tcc tca ccc gcg tct gcc acc ttc ccc	1920
Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro	
625 630 635 640	
gtg tct gtg cag gag ccc ccc acc aag ccg agg ttc acg aca ggc ctc	1968
Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu	
645 650 655	
gtg tat gac acg ctg atg ctg aag cac cag tgc acc tgc ggg agt agc	2016
Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser	
660 665 670	
agc agc cac ccc gag cac gcc ggg agg atc cag agc atc tgg tcc cgc	2064
Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg	
675 680 685	
ctg cag gag acg ggc ctc cgg ggc aaa tgc gag tgc atc cgc gga cgc	2112
Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg	
690 695 700	
aag gcc acc ctg gag gag cta cag acg gtg cac tgc gaa gcc cac acc	2160
Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr	
705 710 715 720	
ctc ctg tat ggc acg aac ccc ctc aac ccg cag aaa ctg gac agt aag	2208
Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys	
725 730 735	
aaa ctt cta ggc tgc ctc gcc tcc gtg ttc gtc ccg ctc cct tgc ggt	2256
Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly	
740 745 750	
ggg gtt ggg gtg gac agt gac acc ata tgg aac gag gtg cac tgc gcg	2304
Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala	
755 760 765	
ggg gca gcc cgc ctg gct gtg ggc tgc gtg gta gag ctg gtc ttc aag	2352
Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys	
770 775 780	
gtg gcc aca ggg gag ctg aag aat ggc ttt gct gtg gtc cgc ccc cct	2400
Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro	
785 790 795 800	
gga aag ctt gcg gag gag agc acg ccc atg ggc ttt tgc tac ttc aac	2448
Gly Lys Leu Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn	
805 810 815	
tcc gtg gcc gtg gca gcc aag ctt ctg cag cag agg ttg agc gtg agc	2496
Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser	
820 825 830	
aag atc ctc atc gtg gac tgg gac gtg cac cat gga aac ggg acc cag	2544
Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln	
835 840 845	
cag gct ttc tac agc gac cct agc gtc ctg tac atg tcc ctc cac cgc	2592
Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg	
850 855 860	
tac gac gat ggg aac ttc ttc cca ggc agc ggg gct cct gat gag gtg	2640
Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val	
865 870 875 880	
ggc aca ggg ccc ggc gtg ggt ttc aac gtc aac atg gct ttc acc ggc	2688
Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly	
885 890 895	
ggc ctg gac ccc ccc atg gga gac gct gag tac ttg gcg gcc ttc aga	2736
Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg	
900 905 910	

09598

acg gtg gtc atg ccg atc gcc agc gag ttt gcc ccg gat gtg gtg ctg	2784
Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu	
915 920 925	
gtg tca tca ggc ttc gat gcc gtg gag ggc cac ccc acc cct ctt ggg	2832
Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly	
930 935 940	
ggc tac aac ctc tcc gcc aga tgc ttc ggg tac ctg acg aag cag ctg	2880
Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu	
945 950 955 960	
atg ggc ctg gct ggc ggc cgg att gtc ctg gcc ctc gag gga ggc cac	2928
Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His	
965 970 975	
gac ctg acc gcc att tgc gac gcc tcg gaa gca tgt gtt tct gcc ttg	2976
Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu	
980 985 990	
ctg gga aac gag ctt gat cct ctc cca gaa aag gtt tta cag caa aga	3024
Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg	
995 1000 1005	
ccc aat gca aac gct gtc cgt tcc atg gag aaa gtc atg gag atc cac	3072
Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His	
1010 1015 1020	
agc aag tac tgg cgc tgc ctg cag cgc aca acc tcc aca gcg tct ctg	3120
Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg	
1025 1030 1035 1040	
tct ctg atc gag gct cag act tgc gag aac gaa gaa gcc gag acg gtc	3168
Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val	
1045 1050 1055	
acc gcc atg gcc tcg ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga	3216
Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg	
1060 1065 1070	
cca gat gag gag ccc atg gaa gag gag ccg ccc ctg tag	3255
Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu	
1075 1080	

<210> 4
 <211> 1084
 <212> PRT
 <213> Artificial

<220>
 <223> Dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

<400> 4
 Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
 1 5 10 15
 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
 20 25 30
 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
 35 40 45
 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
 50 55 60
 Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
 65 70 75 80
 Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
 85 90 95
 His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
 100 105 110

09598

Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
 115 120 125
 Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu
 130 135 140
 Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys
 145 150 155 160
 Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln
 165 170 175
 Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn
 180 185 190
 His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His
 195 200 205
 Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser
 210 215 220
 Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro
 225 230 235 240
 Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu
 245 250 255
 Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
 260 265 270
 Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr
 275 280 285
 Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn
 290 295 300
 Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val
 305 310 315 320
 Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg
 325 330 335
 Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro
 340 345 350
 Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala
 355 360 365
 Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg
 370 375 380
 Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser
 385 390 395 400
 Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His
 405 410 415
 Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly
 420 425 430
 Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg
 435 440 445
 Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg
 450 455 460
 Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu
 465 470 475 480
 Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln
 485 490 495
 Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser
 500 505 510

09598

Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu
 515 520 525
 Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu
 530 535 540
 Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln
 545 550 555 560
 Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val
 565 570 575
 Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln
 580 585 590
 Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr
 595 600 605
 Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His
 610 615 620
 Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro
 625 630 635 640
 Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu
 645 650 655
 Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser
 660 665 670
 Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg
 675 680 685
 Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg
 690 695 700
 Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr
 705 710 715 720
 Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys
 725 730 735
 Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly
 740 745 750
 Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala
 755 760 765
 Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys
 770 775 780
 Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro
 785 790 795 800
 Gly Lys Leu Ala Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn
 805 810 815
 Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser
 820 825 830
 Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln
 835 840 845
 Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg
 850 855 860
 Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val
 865 870 875 880
 Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly
 885 890 895
 Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg
 900 905 910

(13)

09598

Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu
 915 920 925
 Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly
 930 935 940
 Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu
 945 950 955 960
 Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His
 965 970 975
 Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu
 980 985 990
 Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
 995 1000 1005
 Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
 1010 1015 1020
 Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
 1025 1030 1035 1040
 Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
 1045 1050 1055
 Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg
 1060 1065 1070
 Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu
 1075 1080

<210> 5
 <211> 3255
 <212> DNA
 <213> Artificial
 <220>
 <221> CDS
 <222> (1).. (3255)
 <223> Dominant negative mutant (H863L) of human histone deacetylase-4 (HDAC4)
 gene

<400> 5
 atg agc tcc caa agc cat cca gat gga ott tct ggc cga gac cag cca 48
 Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
 1 5 10 15
 gtg gag ctg ctg aat cct gcc cgc gtg aac cac atg ccc ago acg gtg 96
 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
 20 25 30
 gat gtg gcc acg gcg ctg cct ctg caa gtg gcc ccc tgg gca gtg ccc 144
 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
 35 40 45
 atg gac ctg cgc ctg gac cac cag ttc tca ctg cct gtg gca gag ccg 192
 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
 50 55 60
 gcc ctg cgg gag cag cag ctg cag cag gag ctc ctg gcg ctc aag cag 240
 Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
 65 70 75 80
 aag cag cag atc cag agg cag atc ctc atc gct gag ttc cag agg cag 288
 Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
 85 90 95
 cac gag cag ctc tcc cgg cag cac gag gcg cag ctc cac gag cac atc 336
 His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
 100 105 110

09598

aag caa caa cag gag atg ctg gcc atg aag cac cag cag gag ctg ctg Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu 115 120 125	384
gaa cac cag cgg aag ctg gag agg cac cgc cag gag cag gag ctg gag Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu 130 135 140	432
aag cag cac cgg gag cag aag ctg cag cag ctc aag aac aag gag aag Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys 145 150 155 160	480
ggc aaa gag agt gcc gtg gcc agc aca gaa gtg aag atg aag tta caa Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln 165 170 175	528
gaa ttt gtc ctc aat aaa aag aag gcg ctg gcc cac cgg aat ctg aac Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn 180 185 190	576
cac tgc att tcc agc gac cct cgc tac tgg tac ggg aaa acg cag cac His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His 195 200 205	624
agt tcc ctt gac cag agt tct cca ccc cag agc gga gtg tgc acc tcc Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser 210 215 220	672
tat aac cac ccg gtc ctg gga atg tac gac gcc aaa gat gac ttc cct Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro 225 230 235 240	720
ctt agg aaa aca gct tct gaa cgg aat ctg aaa tta cgg tcc agg cta Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu 245 250 255	768
aag cag aaa gtg gcc gaa aga cgg agc agc ccc ctg tta cgc agg aaa Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys 260 265 270	816
gac ggg cca gtg gtc act gct cta aaa aag cgt ccg ttg gat gtc aca Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr 275 280 285	864
gac tcc gcg tgc agc agc gcc cca ggc tcc gga ccc agc tca ccc aac Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn 290 295 300	912
aac agc tcc ggg agc gtc agc gcg gag aac ggt atc gcg ccc gcc gtc Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val 305 310 315 320	960
ccc agc atc ccg gcg gag acg agt ttg gcg cac aga ctt gtg gca cga Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg 325 330 335	1008
gaa ggc tog gcc gct cca ctt ccc ctc tac aca tog cca tcc ttg ccc Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro 340 345 350	1056
aac atc acg ctg ggc ctg cct gcc acc ggc ccc tct gcg ggc acg gcg Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala 355 360 365	1104
ggc cag cag gac acc gag aga ctc acc ott ccc gcc ctc cag cag agg Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg 370 375 380	1152
ctc tcc ctt ttc ccc ggc acc cac ctc act ccc tac ctg agc acc tgc Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser 385 390 395 400	1200
ccc ttg gag cgg gac gga ggg gca gcg cac agc cct ott ctg cag cac Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His 405 410 415	1248

09598

atg gtc tta ctg gag cag cca ccg gca caa gca ccc ctc gtc aca ggc Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly 420 425 430	1296
ctg gga gca ctg ccc ctc cac gca cag tcc ttg gtt ggt gca gac cgg Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg 435 440 445	1344
gtg tcc ccc tcc atc cac aag ctg cgg cag cac cgc cca ctg ggg cgg Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg 450 455 460	1392
acc cag tcg gcc ccg ctg ccc cag aac gcc cag gct ctg cag cac ctg Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu 465 470 475 480	1440
gtc atc cag cag cag cat cag cag ttt ctg gag aaa cac aag cag cag Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln 485 490 495	1488
ttc cag cag cag caa ctg cag atg aac aag atc atc ccc aag cca agc Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser 500 505 510	1536
gag cca gcc cgg cag ccg gag agc cac ccg gag gag acg gag gag gag Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu 515 520 525	1584
ctc cgt gag cac cag gct ctg ctg gac gag ccc tac ctg gac cgg ctg Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu 530 535 540	1632
ccg ggg cag aag gag gcg cac gca cag gcc ggc gtg cag gtg aag cag Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln 545 550 555 560	1680
gag ccc att gag agc gat gag gaa gag gca gag ccc cca cgg gag gtg Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val 565 570 575	1728
gag ccg ggc cag cgc cag ccc agt gag cag gag ctg ctc ttc aga cag Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln 580 585 590	1776
caa gcc ctc ctg ctg gag cag cag cgg atc cac cag ctg agg aac tac Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr 595 600 605	1824
cag gcg tcc atg gag gcc gcc ggc atc ccc gtg tcc ttc ggc ggc cac Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His 610 615 620	1872
agg cct ctg tcc cgg gcg cag tcc tca ccc gcg tct gcc acc ttc ccc Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro 625 630 635 640	1920
gtg tct gtg cag gag ccc ccc acc aag ccg agg ttc acg aca ggc ctc Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu 645 650 655	1968
gtg tat gac acg ctg atg ctg aag cac cag tgc acc tgc ggg agt agc Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser 660 665 670	2016
agc agc cac ccc gag cac gcc ggg agg atc cag agc atc tgg tcc cgc Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg 675 680 685	2064
ctg cag gag acg ggc ctc cgg ggc aaa tgc gag tgc atc cgc gga cgc Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg 690 695 700	2112
aag gcc acc ctg gag gag cta cag acg gtg cac tgc gaa gcc cac acc Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr 705 710 715 720	2160

705	710	715	09598	720	
ctc ctg tat ggc acg aac ccc ctc aac cgg cag aaa ctg gac agt aag Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys 725 730 735					2208
aaa ott cta ggc tcg ctc gcc tcc gtg ttc gtc cgg ctc cct tgc ggt Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly 740 745 750					2256
ggt gtt ggg gtg gac agt gac acc ata tgg aac gag gtg cac tcg gcg Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala 755 760 765					2304
ggg gca gcc cgc ctg gct gtg ggc tgc gtg gta gag ctg gtc ttc aag Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys 770 775 780					2352
gtg gcc aca ggg gag ctg aag aat ggc ttt gct gtg gtc cgc ccc cct Val Ala Thr Gly Glu Lys Asn Gly Phe Ala Val Val Arg Pro Pro 785 790 800					2400
gga cac cat gcg gag gag agc acg ccc atg ggc ttt tgc tac ttc aac Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn 805 810 815					2448
tcc gtg gcc gtg gca gcc aag ctt ctg cag cag agg ttg agc gtg agc Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser 820 825 830					2496
aag atc ctc atc gtg gac tgg gac gtg cac cat gga aac ggg acc cag Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln 835 840 845					2544
cag gct ttc tac agc gac cct agc gtc ctg tac atg tcc ctc ctt cgc Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu Leu Arg 850 855 860					2592
tac gac gat ggg aac ttc ttc cca ggc agc ggg gct cct gat gag gtg Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val 865 870 875 880					2640
ggc aca ggg ccc ggc gtg ggt ttc aac gtc aac atg gct ttc acc ggc Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly 885 890 895					2688
ggc ctg gac ccc ccc atg gga gac gct gag tac ttg gcg gcc ttc aga Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg 900 905 910					2736
acg gtg gtc atg ccg atc gcc agc gag ttt gcc ccg gat gtg gtg ctg Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu 915 920 925					2784
gtg tca tca ggc ttc gat gcc gtg gag ggc cac ccc acc cct ctt ggg Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly 930 935 940					2832
ggc tac aac ctc tcc gcc aga tgc ttc ggg tac ctg acg aag cag ctg Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu 945 950 955 960					2880
atg ggc ctg gct ggc ggc cgg att gtc ctg gcc ctc gag gga ggc cac Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His 965 970 975					2928
gac ctg acc gcc att tgc gac gcc tcg gaa gca tgt gtt tct gcc ttg Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu 980 985 990					2976
ctg gga aac gag ctt gat cct ctc cca gaa aag gtt tta cag caa aga Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg 995 1000 1005					3024
ccc aat gca aac gct gtc cgt tcc atg gag aaa gtc atg gag atc cac					3072

09598

Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
1010 1015 1020

agc aag tac tgg cgc tgc ctg cag cgc aca acc tcc aca gcg ggg cgt 3120
Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
1025 1030 1035 1040

tct ctg atc gag gct cag act tgc gag aac gaa gaa gcc gag acg gtc 3168
Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
1045 1050 1055

acc gcc atg gcc tgc ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga 3216
Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg
1060 1065 1070

cca gat gag gag ccc atg gaa gag gag ccg ccc ctg tag 3255
Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu
1075 1080

<210> 6
<211> 1084
<212> PRT
<213> Homo sapiens

<220>
<223> Dominant negative mutant (H863L) of human histone deacetylase-4 (HDAC4)
gene

<400> 6
Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
1 5 10 15

Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
20 25 30

Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
35 40 45

Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
50 55 60

Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Ala Leu Lys Gln
65 70 75 80

Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
85 90 95

His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
100 105 110

Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
115 120 125

Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu
130 135 140

Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys
145 150 155 160

Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln
165 170 175

Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn
180 185 190

His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His
195 200 205

Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser
210 215 220

Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro
225 230 235 240

09598

Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu
245 250 255

Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
260 265 270

Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr
275 280 285

Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn
290 295 300

Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val
305 310 315 320

Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg
325 330 335

Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro
340 345 350

Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala
355 360 365

Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg
370 375 380

Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser
385 390 395 400

Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His
405 410 415

Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly
420 425 430

Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg
435 440 445

Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg
450 455 460

Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu
465 470 475 480

Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln
485 490 495

Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser
500 505 510

Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu
515 520 525

Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu
530 535 540

Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln
545 550 555 560

Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val
565 570 575

Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln
580 585 590

Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr
595 600 605

Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His
610 615 620

Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro
625 630 635 640

09598

Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu
645 650 655

Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser
660 665 670

Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg
675 680 685

Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg
690 695 700

Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr
705 710 715 720

Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys
725 730 735

Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly
740 745 750

Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala
755 760 765

Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys
770 775 780

Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro
785 790 795 800

Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn
805 810 815

Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser
820 825 830

Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln
835 840 845

Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu Leu Arg
850 855 860

Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val
865 870 875 880

Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly
885 890 895

Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg
900 905 910

Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu
915 920 925

Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly
930 935 940

Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu
945 950 955 960

Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His
965 970 975

Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu
980 985 990

Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
995 1000 1005

Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
1010 1015 1020

Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
1025 1030 1035 1040

09598

Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
1045 1050 1055

Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg
1060 1065 1070

Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu
1075 1080

<210> 7
<211> 1743
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (43)..(1176)
<223> human histone deacetylase-8 (HDAC8) gene

<400> 7
gccagatctg gaaggtggct gcggaacggg ttttaagogga ag atg gag gag ccg 54
Met Glu Glu Pro
1

gag gaa ccg gcg gac agt ggg cag tcg ctg gtc ccg gtt tat atc tat 102
Glu Glu Pro Ala Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr
5 10 15 20

agt ccc gag tat gtc agt atg tgt gac tcc ctg gcc aag atc ccc aaa 150
Ser Pro Glu Tyr Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys
25 30 35

cgg gcc agt atg gtg cat tct ttg att gaa gca tat gca ctg cat aag 198
Arg Ala Ser Met Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys
40 45 50

cag atg agg ata gtt aag cct aaa gtg gcc tcc atg gag gag atg gcc 246
Gln Met Arg Ile Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala
55 60 65

acc ttc cac act gat gct tat ctg cag cat ctc cag aag gtc agc caa 294
Thr Phe His Thr Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln
70 75 80

gag ggc gat gat gat cat ccg gac tcc ata gaa tat ggg cta ggt tat 342
Glu Gly Asp Asp Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr
85 90 95 100

gac tgc cca gcc act gaa ggg ata ttt gac tat gca gca gct ata gga 390
Asp Cys Pro Ala Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly
105 110 115

ggg gct acg atc aca gct gcc caa tgc ctg att gac gga atg tgc aaa 438
Gly Ala Thr Ile Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys
120 125 130

gta gca att aac tgg tct gga ggg tgg cat cat gca aag aaa gat gaa 486
Val Ala Ile Asn Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu
135 140 145

gca tct ggt ttt tgt tat ctc aat gat gct gtc ctg gga ata tta cga 534
Ala Ser Gly Phe Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg
150 155 160

ttg cga cgg aaa ttt gag cgt att ctc tac gtg gat ttg gat ctg cac 582
Leu Arg Arg Lys Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His
165 170 175 180

cat gga gat ggt gta gaa gac gca ttc agt ttc acc tcc aaa gtc atg 630
His Gly Asp Gly Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met
185 190 195

acc gtg tcc ctg cac aaa ttc tcc cca gga ttt ttc cca gga aca ggt 678
Thr Val Ser Leu His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly

200	205	09598 210													
gac gtg tct gat gtt ggc cta ggg aag gga cgg tac tac agt gta aat Asp Val Ser Asp Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn 215 220 225			726												
gtg ccc att cag gat ggc ata caa gat gaa aaa tat tac cag atc tgt Val Pro Ile Gln Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys 230 235 240			774												
gaa agt gta cta aag gaa gta tac caa gcc ttt aat ccc aaa gca gtg Glu Ser Val Leu Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val 245 250 255 260			822												
gtc tta cag ctg gga gct gac aca ata gct ggg gat ccc atg tgc tcc Val Leu Gln Leu Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser 265 270 275			870												
ttt aac atg act cca gtg gga att ggc aag tgt ctt aag tac atc ctt Phe Asn Met Thr Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu 280 285 290			918												
caa tgg cag ttg gca aca ctc att ttg gga gga gga ggc tat aac ctt Gln Trp Gln Leu Ala Thr Leu Ile Leu Gly Gly Gly Tyr Asn Leu 295 300 305			966												
gcc aac acg gct cga tgc tgg aca tac ttg acc ggg gtc atc cta ggg Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly 310 315 320			1014												
aaa aca cta tcc tct gag atc cca gat cat gag ttt ttc aca gca tat Lys Thr Leu Ser Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr 325 330 335 340			1062												
ggt cct gat tat gtg ctg gaa atc acg cca agc tgc cgg cca gac cgc Gly Pro Asp Tyr Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg 345 350 355			1110												
aat gag ccc cac cga atc caa caa atc ctc aac tac atc aaa ggg aat Asn Glu Pro His Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn 360 365 370			1158												
ctg aag cat gtg gtc tag ttgacagaaa gagatcaggt ttccagagct Leu Lys His Val Val 375			1206												
gaggagtggg gcctataatg aagacagcgt gtttatgcaa gcagtttgtg gaatttgtga			1266												
ctgcagggaa aatttgaaag aaattacttc ctgaaaattt ccaaggggca tcaagtggca			1326												
gctggcttcc tggggtgaag aggcaggcac ccagaggtcc tcaactggac ctagggggaag			1386												
aaggagatat cccacattta aagttottat ttataaaaaac acacacacac aaatgaaatt			1446												
tttaattttt gaaaattatt tttaagcgaa ttggggaggg gagtatttta atcatcttaa			1506												
atgaaacaga tcagaagctg gatgagagca gtcaccagtt ttaggggag gaggcagctg			1566												
agaggcaggg tttgggcctc aggaccatcc aggtggagcc ctgggagaga gggactgat			1626												
cagcagactg ggaggtgggg agaagtccgc tgggtgtgtt ttagtgttat atatctttgg			1686												
tttttttaat aaaatctttg aaaacctaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa			1743												
 <210> 8															
<211> 377															
<212> PRT															
<213> Homo sapiens															
 <400> 8															
Met	Glu	Glu	Pro	Glu	Glu	Pro	Ala	Asp	Ser	Gly	Gln	Ser	Leu	Val	Pro
1				5				10					15		

09598

Val Tyr Ile Tyr Ser Pro Glu Tyr Val Ser Met Cys Asp Ser Leu Ala
20 25 30

Lys Ile Pro Lys Arg Ala Ser Met Val His Ser Leu Ile Glu Ala Tyr
35 40 45

Ala Leu His Lys Gln Met Arg Ile Val Lys Pro Lys Val Ala Ser Met
50 55 60

Glu Glu Met Ala Thr Phe His Thr Asp Ala Tyr Leu Gln His Leu Gln
65 70 75 80

Lys Val Ser Gln Glu Gly Asp Asp Asp His Pro Asp Ser Ile Glu Tyr
85 90 95

Gly Leu Gly Tyr Asp Cys Pro Ala Thr Glu Gly Ile Phe Asp Tyr Ala
100 105 110

Ala Ala Ile Gly Gly Ala Thr Ile Thr Ala Ala Gln Cys Leu Ile Asp
115 120 125

Gly Met Cys Lys Val Ala Ile Asn Trp Ser Gly Gly Trp His His Ala
130 135 140

Lys Lys Asp Glu Ala Ser Gly Phe Cys Tyr Leu Asn Asp Ala Val Leu
145 150 155 160

Gly Ile Leu Arg Leu Arg Arg Lys Phe Glu Arg Ile Leu Tyr Val Asp
165 170 175

Leu Asp Leu His His Gly Asp Gly Val Glu Asp Ala Phe Ser Phe Thr
180 185 190

Ser Lys Val Met Thr Val Ser Leu His Lys Phe Ser Pro Gly Phe Phe
195 200 205

Pro Gly Thr Gly Asp Val Ser Asp Val Gly Leu Gly Lys Gly Arg Tyr
210 215 220

Tyr Ser Val Asn Val Pro Ile Gln Asp Gly Ile Gln Asp Glu Lys Tyr
225 230 235 240

Tyr Gln Ile Cys Glu Ser Val Leu Lys Glu Val Tyr Gln Ala Phe Asn
245 250 255

Pro Lys Ala Val Val Leu Gln Leu Gly Ala Asp Thr Ile Ala Gly Asp
260 265 270

Pro Met Cys Ser Phe Asn Met Thr Pro Val Gly Ile Gly Lys Cys Leu
275 280 285

Lys Tyr Ile Leu Gln Trp Gln Leu Ala Thr Leu Ile Leu Gly Gly Gly
290 295 300

Gly Tyr Asn Leu Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly
305 310 315 320

09598

Val Ile Leu Gly Lys Thr Leu Ser Ser Glu Ile Pro Asp His Glu Phe
325 330 335

Phe Thr Ala Tyr Gly Pro Asp Tyr Val Leu Glu Ile Thr Pro Ser Cys
340 345 350

Arg Pro Asp Arg Asn Glu Pro His Arg Ile Gln Gln Ile Leu Asn Tyr
355 360 365

Ile Lys Gly Asn Leu Lys His Val Val

<210> 9
<211> 1449
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1449)
<223> human histone deacetylase-1 (HDAC1) gene

<400> 9
atg gcg cag acg cag ggc acc cgg agg aaa gtc tgt tac tac tac gac 48
Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
1 5 10 15
ggg gat gtt gga aat tac tat tat gga caa ggc cac cca atg aag cct 96
Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
20 25 30
cac cga atc cgc atg act cat aat ttg ctg ctc aac tat ggt ctc tac 144
His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
35 40 45
cga aaa atg gaa atc tat cgc cct cac aaa gcc aat gct gag gag atg 192
Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
50 55 60
acc aag tac cac agc gat gac tac att aaa ttc ttg cgc tcc atc cgt 240
Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
65 70 75 80
cca gat aac atg tcg gag tac agc aag cag atg cag aga ttc aac gtt 288
Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
85 90 95
ggt gag gac tgt cca gta ttc gat ggc ctg ttt gag ttc tgt cag ttg 336
Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
100 105 110
tct act ggt ggt tct gtg gca agt gct gtg aaa ctt aat aag cag cag 384
Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
115 120 125
acg gac atc gct gtg aat tgg gct ggg ggc ctg cac cat gca aag aag 432
Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys
130 135 140
tcc gag gca tct ggc ttc tgt tac gtc aat gat atc gtc ttg gcc atc 480
Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
145 150 155 160
ctg gaa ctg cta aag tat cac cag agg gtg ctg tac att gac att gat 528
Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
165 170 175
att cac cat ggt gac ggc gtg gaa gag gcc ttc tac acc acg gac cgg 576
Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
180 185 190

(24)

09598

gtc atg act gtg tcc ttt cat aag tat gga gag tac ttc cca gga act Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr 195 200 205	624
ggg gac cta cgg gat atc ggg gct ggc aaa ggc aag tat tat gct gtt Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val 210 215 220	672
aac tac ccg ctc cga gac ggg att gat gac gag tcc tat gag gcc att Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile 225 230 235 240	720
ttc aag ccg gtc atg tcc aaa gta atg gag atg ttc cag cct agt gcg Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala 245 250 255	768
gtg gtc tta cag tgt ggc tca gac tcc cta tct ggg gat cgg tta ggt Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly 260 265 270	816
tgc ttc aat cta act atc aaa gga cac gcc aag tgt gtg gaa ttt gtc Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val 275 280 285	864
aag agc ttt aac ctg cct atg ctg atg ctg gga ggc ggt ggt tac acc Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr 290 295 300	912
att cgt aac gtt gcc cgg tgc agg aca tat gag aca gct gtg gcc ctg Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu 305 310 315 320	960
gat acg gag atc cct aat gag ctt cca tac aat gac tac ttt gaa tac Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr 325 330 335	1008
ttt gga cca gat ttc aag ctc cac atc agt cct tcc aat atg act aac Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn 340 345 350	1056
cag aac acg aat gag tac ctg gag aag atc aaa cag cga ctg ttt gag Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu 355 360 365	1104
aac ctt aga atg ctg ccg cac gca cct ggg gtc caa atg cag gcg att Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile 370 375 380	1152
cct gag gac gcc atc cct gag gag agt ggc gat gag gac gaa gac gac Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp 385 390 395 400	1200
cct gac aag cgc atc tgc atc tgc tcc tct gac aaa cga att gcc tgt Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys 405 410 415	1248
gag gaa gag ttc tcc gat tct gaa gag gag gga gag ggg gcc cgc aag Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys 420 425 430	1296
aac tct tcc aac ttc aaa aaa gcc aag aga gtc aaa aca gag gat gaa Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu 435 440 445	1344
aaa gag aaa gac cca gag gag aag aaa gaa gtc acc gaa gag gag aaa Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys 450 455 460	1392
acc aag gag gag aag cca gaa gcc aaa ggg gtc aag gag gag gtc aag Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys 465 470 475 480	1440
ttg gcc tga Leu Ala	1449

<210> 10
 <211> 482
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
 1 5 10 15

Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
 20 25 30

His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
 35 40 45

Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
 50 55 60

Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
 65 70 75 80

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
 85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
 100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
 115 120 125

Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys
 130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
 145 150 155 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
 165 170 175

Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
 180 185 190

Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
 195 200 205

Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
 210 215 220

Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile
 225 230 235 240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala
 245 250 255

Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly
 260 265 270

09598

Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val
275 280 285

Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr
290 295 300

Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu
305 310 315 320

Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr
325 330 335

Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn
340 345 350

Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu
355 360 365

Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile
370 375 380

Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp
385 390 395 400

Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys
405 410 415

Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys
420 425 430

Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
435 440 445

Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys
450 455 460

Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
465 470 475 480

Leu Ala

<210> 11

<211> 1449

<212> DNA

<213> Artificial

<220>

<221> CDS

<222> (1)..(1449)

<223> Dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 11

atg gcg cag acg cag ggc acc cgg agg aaa gtc tgt tac tac tac gac 48
Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
1 5 10 15

ggg gat gtt gga aat tac tat tat gga caa ggc cac cca atg aag cct 96

(27)

09598

Gly Asp Val	Gly Asn Tyr Tyr Tyr	Gly Gln Gly His Pro	Met Lys Pro	
20		25	30	
cac cga atc cgc atg act cat aat ttg ctg ctc aac tat ggt ctc tac	144			
His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr				
35	40	45		
cga aaa atg gaa atc tat cgc cct cac aaa gcc aat gct gag gag atg	192			
Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met				
50	55	60		
acc aag tac cac agc gat gac tac att aaa ttc ttg cgc tcc atc cgt	240			
Thr Lys Tyr His Ser Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg				
65	70	75	80	
cca gat aac atg tgc gag tac agc aag cag atg cag aga ttc aac gtt	288			
Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val				
85	90	95		
ggt gag gac tgt cca gta ttc gat ggc ctg ttt gag ttc tgt cag ttg	336			
Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu				
100	105	110		
tct act ggt ggt tct gtg gca agt gct gtg aaa ctt aat aag cag cag	384			
Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln				
115	120	125		
acg gac atc gct gtg aat tgg gct ggg ggc ctg aag ctt gca aag aag	432			
Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys				
130	135	140		
tcc gag gca tct ggc ttc tgt tac gtc aat gat atc gtc ttg gcc atc	480			
Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile				
145	150	155	160	
ctg gaa ctg cta aag tat cac cag agg gtg ctg tac att gac att gat	528			
Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp				
165	170	175		
att cac cat ggt gac ggc gtg gaa gag gcc ttc tac acc acg gac cgg	576			
Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg				
180	185	190		
gtc atg act gtg tcc ttt cat aag tat gga gag tac ttc cca gga act	624			
Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr				
195	200	205		
ggg gac cta cgg gat atc ggg gct ggc aaa ggc aag tat tat gct gtt	672			
Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val				
210	215	220		
aac tac ccg ctc cga gac ggg att gat gac gag tcc tat gag gcc att	720			
Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile				
225	230	235	240	
ttc aag ccg gtc atg tcc aaa gta atg gag atg ttc cag cct agt gcg	768			
Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala				
245	250	255		
gtg gtc tta cag tgt ggc tca gac tcc cta tct ggg gat cgg tta ggt	816			
Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly				
260	265	270		
tgc ttc aat cta act atc aaa gga cac gcc aag tgt gtg gaa ttt gtc	864			
Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val				
275	280	285		
aag agc ttt aac ctg cct atg ctg atg ctg gga ggc ggt ggt tac acc	912			
Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr				
290	295	300		
att cgt aac gtt gcc cgg tgc agg aca tat gag aca gct gtg gcc ctg	960			
Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu				
305	310	315	320	

09598

gat acg gag atc cct aat gag ctt cca tac aat gac tac ttt gaa tac Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr 325 330 335	1008
ttt gga cca gat ttc aag ctc cac atc agt cct tcc aat atg act aac Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn 340 345 350	1056
cag aac acg aat gag tac ctg gag aag atc aaa cag cga ctg ttt gag Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu 355 360 365	1104
aac ctt aga atg ctg cgg cac gca cct ggg gtc caa atg cag gcg att Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile 370 375 380	1152
cct gag gac gcc atc cct gag gag agt ggc gat gag gac gaa gac gac Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp 385 390 395 400	1200
cct gac aag cgc atc tog atc tgc tcc tct gac aaa cga att gcc tgt Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys 405 410 415	1248
gag gaa gag ttc tcc gat tct gaa gag gag gga gag ggg ggc cgc aag Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys 420 425 430	1296
aac tct tcc aac ttc aaa aaa gcc aag aga gtc aaa aca gag gat gaa Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu 435 440 445	1344
aaa gag aaa gac cca gag gag aag aaa gaa gtc acc gaa gag gag aaa Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys 450 455 460	1392
acc aag gag gag aag cca gaa gcc aaa ggg gtc aag gag gag gtc aag Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys 465 470 475 480	1440
ttg gcc tga Leu Ala	1449

<210> 12
 <211> 482
 <212> PRT
 <213> Artificial

<220>
 <223> Dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 12
 Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Asp
 1 5 10 15

Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
 20 25 30

His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
 35 40 45

Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
 50 55 60

Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
 65 70 75 80

09598

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
115 120 125

Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys
130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
145 150 155 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
165 170 175

Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
180 185 190

Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
195 200 205

Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
210 215 220

Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile
225 230 235 240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala
245 250 255

Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly
260 265 270

Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val
275 280 285

Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr
290 295 300

Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu
305 310 315 320

Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr
325 330 335

Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn
340 345 350

Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu
355 360 365

Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile
370 375 380

09598

Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp
385 390 395 400

Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys
405 410 415

Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys
420 425 430

Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
435 440 445

Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys
450 455 460

Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
465 470 475 480

Leu Ala

<210> 13
<211> 1449
<212> DNA
<213> Artificial

<220>
<221> CDS
<222> (1)..(1449)
<223> Dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1)
gene

<400> 13
atg gcg cag acg cag ggc acc cgg agg aaa gtc tgt tac tac tac gac 48
Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Asp
1 5 10 15
ggg gat gtt gga aat tac tat tat gga caa ggc cac cca atg aag cct 96
Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
20 25 30
cac cga atc cgc atg act cat aat ttg ctg ctc aac tat ggt ctc tac 144
His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
35 40 45
cga aaa atg gaa atc tat cgc cct cac aaa gcc aat gct gag gag atg 192
Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
50 55 60
acc aag tac cac agc gat gac tac att aaa ttc ttg cgc tcc atc cgt 240
Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
65 70 75 80
cca gat aac atg tcg gag tac agc aag cag atg cag aga ttc aac gtt 288
Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
85 90 95
ggg gat gac tgt cca gta ttc gat ggc ctg ttt gag ttc tgt cag ttg 336
Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
100 105 110
tct act ggt ggt tct gtg gca agt gct gtg aaa ctt aat aag cag cag 384
Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
115 120 125
acg gac atc gct gtg aat tgg gct ggg ggc ctg cac cat gca aag aag 432
Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys

(31)

130	135	140	
tcc gag gca tct ggc ttc tgt tac gtc aat gat atc gtc ttg gcc atc Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile 145 150 155 160			480
ctg gaa ctg cta aag tat cac cag agg gtg ctg tac att gac att gat Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp 165 170 175			528
att cac cat ggt gac ggc gtg gaa gag gcc ttc tac acc acg gac cgg Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg 180 185 190			576
gtc atg act gtg tcc ttt ctt aag tat gga gag tac ttc cca gga act Val Met Thr Val Ser Phe Leu Lys Tyr Gly Glu Tyr Phe Pro Gly Thr 195 200 205			624
ggg gac cta cgg gat atc ggg gct ggc aaa ggc aag tat tat gct gtt Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val 210 215 220			672
aac tac ccg ctc cga gac ggg att gat gac gag tcc tat gag gcc att Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile 225 230 235 240			720
ttc aag ccg gtc atg tcc aaa gta atg gag atg ttc cag cct agt gcg Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala 245 250 255			768
gtg gtc tta cag tgt ggc tca gac tcc cta tct ggg gat cgg tta ggt Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly 260 265 270			816
tgc ttc aat cta act atc aaa gga cac gcc aag tgt gtg gaa ttt gtc Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val 275 280 285			864
aag agc ttt aac ctg cct atg ctg atg ctg gga ggc ggt ggt tac acc Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr 290 295 300			912
att cgt aac gtt gcc cgg tgc agg aca tat gag aca gct gtg gcc ctg Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu 305 310 315 320			960
gat acg gag atc cct aat gag ctt cca tac aat gac tac ttt gaa tac Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr 325 330 335			1008
ttt gga cca gat ttc aag ctc cac atc agt cct tcc aat atg act aac Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn 340 345 350			1056
cag aac acg aat gag tac ctg gag aag atc aaa cag cga ctg ttt gag Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu 355 360 365			1104
aac ctt aga atg ctg ccg cac gca cct ggg gtc caa atg cag gcg att Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile 370 375 380			1152
cct gag gac gcc atc cct gag gag agt ggc gat gag gac gaa gac gac Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp 385 390 395 400			1200
cct gac aag cgc atc tgc atc tgc tcc tct gac aaa cga att gcc tgt Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys 405 410 415			1248
gag gaa gag ttc tcc gat tct gaa gag gag gga gag ggg ggc cgc aag Glu Glu Glu Phe Ser Asp Ser Glu Glu Gly Glu Gly Gly Arg Lys 420 425 430			1296
aac tct tcc aac ttc aaa aaa gcc aag aga gtc aaa aca gag gat gaa			1344

09598

Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
 435 440 445

aaa gag aaa gac cca gag gag aag aaa gaa gtc acc gaa gag gag aaa 1392
 Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys
 450 455 460

acc aag gag gag aag cca gaa gcc aaa ggg gtc aag gag gag gtc aag 1440
 Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
 465 470 475 480

ttg gcc tga 1449
 Leu Ala

<210> 14
 <211> 482
 <212> PRT
 <213> Artificial

<220>
 <223> Dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 14
 Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
 1 5 10 15

Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
 20 25 30

His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
 35 40 45

Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
 50 55 60

Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
 65 70 75 80

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
 85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
 100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
 115 120 125

Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys
 130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
 145 150 155 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
 165 170 175

Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
 180 185 190

Val Met Thr Val Ser Phe Leu Lys Tyr Gly Glu Tyr Phe Pro Gly Thr

195

200

205

Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
 210 215 220
 Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile
 225 230 235 240
 Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala
 245 250 255
 Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly
 260 265 270
 Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val
 275 280 285
 Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr
 290 295 300
 Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu
 305 310 315 320
 Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr
 325 330 335
 Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn
 340 345 350
 Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu
 355 360 365
 Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile
 370 375 380
 Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp
 385 390 395 400
 Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys
 405 410 415
 Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Arg Lys
 420 425 430
 Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
 435 440 445
 Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys
 450 455 460
 Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
 465 470 475 480
 Leu Ala

<210> 15
 <211> 1287
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1287)
 <223> human histone deacetylase-3 (HDAC3) gene

<400> 15

atg gcc aag acc gtg gcc tat ttc tac gac ccc gac gtg ggc aac ttc Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe 1 5 10 15	48
cac tac gga gct gga cac cct atg aag ccc cat cgc ctg gca ttg acc His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr 20 25 30	96
cat agc ctg gtc ctg cat tac ggt ctc tat aag aag atg atc gtc ttc His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe 35 40 45	144
aag cca tac cag gcc tcc caa cat gac atg tgc cgc ttc cac tcc gag Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu 50 55 60	192
gac tac att gac ttc ctg cag aga gtc agc ccc acc aat atg caa ggc Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly 65 70 75 80	240
ttc acc aag agt ctt aat gcc ttc aac gta ggc gat gac tgc cca gtg Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val 85 90 95	288
ttt ccc ggg ctc ttt gag ttc tgc tgc cgt tac aca ggc gca tct ctg Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu 100 105 110	336
caa gga gca acc cag ctg aac aac aag atc tgt gat att gcc att aac Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn 115 120 125	384
tgg gct ggt ggt ctg cac cat gcc aag aag ttt gag gcc tct ggc ttc Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe 130 135 140	432
tgc tat gtc aac gac att gtg att ggc atc ctg gag ctg ctc aag tac Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr 145 150 155 160	480
cac cct cgg gtg ctc tac att gac att gac atc cac cat ggt gac ggc His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly 165 170 175	528
gtt caa gaa gct ttc tac ctc act gac cgg gtc atg acg gtg tcc ttc Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe 180 185 190	576
cac aaa tac gga aat tac ttc ttc cct ggc aca ggt gac atg tat gaa His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu 195 200 205	624
gtc ggg gca gag agt ggc cgc tac tac tgt ctg aac gtg ccc ctg cgg Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg 210 215 220	672
gat ggc att gat gac cag agt tac aag cac ctt ttc cag cgg gtt atc Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile 225 230 235 240	720
aac cag gta gtg gac ttc tac caa ccc acg tgc att gtg ctc cag tgt Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys 245 250 255	768

09598

gga gct gac tct ctg ggc tgt gat cga ttg ggc tgc ttt aac ctc agc Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser 260 265 270	816
atc cga ggg cat ggg gaa tgc gtt gaa tat gtc aag agc ttc aat atc Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile 275 280 285	864
cct cta ctc gtg ctg ggt ggt ggt ggt tat act gtc cga aat gtt gcc Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala 290 295 300	912
cgc tgc tgg aca tat gag aca tgc ctg ctg gta gaa gag gcc att agt Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser 305 310 315 320	960
gag gag ctt ccc tat agt gaa tac ttc gag tac ttt gcc cca gac ttc Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe 325 330 335	1008
aca ctt cat cca gat gtc agc acc cgc atc gag aat cag aac tca cgc Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg 340 345 350	1056
cag tat ctg gac cag atc ctc cag aca atc ttt gaa aac ctg aag atg Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met 355 360 365	1104
ctg aac cat gca cct agt gtc cag att cat gac gtg cct gca gac ctc Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu 370 375 380	1152
ctg acc tat gac agg act gat gag gct gat gca gag gag agg ggt cct Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro 385 390 395 400	1200
gag gag aac tat agc agg cca gag gca ccc aat gag ttc tat gat gga Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly 405 410 415	1248
gac cat gac aat gac aag gaa agc gat gtg gag att taa Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile 420 425	1287

<210> 16
 <211> 428
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
 1 5 10 15

His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
 20 25 30

His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
 35 40 45

Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
 50 55 60

Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
 65 70 75 80

Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
 85 90 95

09598

Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
100 105 110

Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
115 120 125

Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe
130 135 140

Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
145 150 155 160

His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
165 170 175

Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
180 185 190

His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu
195 200 205

Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg
210 215 220

Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile
225 230 235 240

Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys
245 250 255

Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser
260 265 270

Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile
275 280 285

Pro Leu Leu Val Leu Gly Gly Gly Gly Tyr Thr Val Arg Asn Val Ala
290 295 300

Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser
305 310 315 320

Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe
325 330 335

Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg
340 345 350

Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met
355 360 365

Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu
370 375 380

Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro
385 390 395 400

09598

Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly
405 410 415

Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile
420 425

<210> 17
<211> 1287
<212> DNA
<213> Artificial

<220>
<221> CDS
<222> (1)..(1287)
<223> Dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 17
atg gcc aag acc gtg gcc tat ttc tac gac ccc gac gtg ggc aac ttc 48
Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
1 5 10 15
cac tac gga gct gga cac cct atg aag ccc cat cgc ctg gca ttg acc 96
His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
20 25 30
cat agc ctg gtc ctg cat tac ggt ctc tat aag aag atg atc gtc ttc 144
His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
35 40 45
aag cca tac cag gcc tcc caa cat gac atg tgc cgc ttc cac tcc gag 192
Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
50 55 60
gac tac att gac ttc ctg cag aga gtc agc ccc acc aat atg caa ggc 240
Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65 70 75 80
ttc acc aag agt ctt aat gcc ttc aac gta ggc gat gac tgc cca gtg 288
Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
85 90 95
ttt ccc ggg ctc ttt gag ttc tgc tgc cgt tac aca ggc gca tct ctg 336
Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
100 105 110
caa gga gca acc cag ctg aac aac aag atc tgt gat att gcc att aac 384
Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
115 120 125
tgg gct ggt ggt ctg aag ctt gcc aag aag ttt gag gcc tct ggc ttc 432
Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys Phe Glu Ala Ser Gly Phe
130 135 140
tgc tat gtc aac gac att gtg att ggc atc ctg gag ctg ctc aag tac 480
Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
145 150 155 160
cac cct cgg gtg ctc tac att gac att gac atc cac cat ggt gac ggc 528
His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
165 170 175
gtt caa gaa gct ttc tac ctc act gac cgg gtc atg acg gtg tcc ttc 576
Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
180 185 190
cac aaa tac gga aat tac ttc ttc cct ggc aca ggt gac atg tat gaa 624
His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu
195 200 205
gtc ggg gca gag agt ggc cgc tac tac tgt ctg aac gtg ccc ctg cgg 672
Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg

(38)

210

215

220

gat ggc att gat gac cag agt tac aag cac ctt ttc cag ccg gtt atc 720
Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile
225 230 235 240

aac cag gta gtg gac ttc tac caa ccc acg tgc att gtg ctc cag tgt 768
Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys
245 250 255

gga got gac tot ctg ggc tgt gat cga ttg ggc tgc ttt aac ctc agc 816
Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser
260 265 270

atc cga ggg cat ggg gaa tgc gtt gaa tat gtc aag agc ttc aat atc 864
Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile
275 280 285

cct cta ctc gtg ctg ggt ggt ggt ggt tat act gtc cga aat gtt gcc 912
Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala
290 295 300

cgc tgc tgg aca tat gag aca tgc ctg ctg gta gaa gag gcc att agt 960
Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser
305 310 315 320

gag gag ctt ccc tat agt gaa tac ttc gag tac ttt gcc cca gac ttc 1008
Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe
325 330 335

aca ctt cat cca gat gtc agc acc cgc atc gag aat cag aac tca cgc 1056
Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg
340 345 350

cag tat ctg gac cag atc ctc cag aca atc ttt gaa aac ctg aag atg 1104
Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met
355 360 365

ctg aac cat gca cct agt gtc cag att cat gac gtg cct gca gac ctc 1152
Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu
370 375 380

ctg acc tat gac agg act gat gag gct gat gca gag gag agg ggt cct 1200
Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro
385 390 395 400

gag gag aac tat agc agg cca gag gca ccc aat gag ttc tat gat gga 1248
Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly
405 410 415

gac cat gac aat gac aag gaa agc gat gtg gag att taa 1287
Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile
420 425

<210> 18
<211> 428
<212> PRT
<213> Artificial

<220>
<223> Dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 18
Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
1 5 10 15

His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
20 25 30

His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
35 40 45

09598

Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
50 55 60

Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65 70 75 80

Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
85 90 95

Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
100 105 110

Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
115 120 125

Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys Phe Glu Ala Ser Gly Phe
130 135 140

Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
145 150 155 160

His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
165 170 175

Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
180 185 190

His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu
195 200 205

Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg
210 215 220

Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile
225 230 235 240

Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys
245 250 255

Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser
260 265 270

Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile
275 280 285

Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala
290 295 300

Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser
305 310 315 320

Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe
325 330 335

Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg

(40)

340

345

09598
350

Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met
355 360 365

Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu
370 375 380

Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro
385 390 395 400

Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly
405 410 415

Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile
420 425

<210> 19
<211> 1287
<212> DNA
<213> Artificial

<220>
<221> CDS
<222> (1)..(1287)
<223> Dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3)
gene

<400> 19
atg gcc aag acc gtg gcc tat ttc tac gac ccc gac gtg ggc aac ttc 48
Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
1 5 10 15
cac tac gga gct gga cac cct atg aag ccc cat cgc ctg gca ttg acc 96
His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
20 25 30
cat agc ctg gtc ctg cat tac ggt ctc tat aag aag atg atc gtc ttc 144
His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
35 40 45
aag cca tac cag gcc tcc caa cat gac atg tgc cgc ttc cac tcc gag 192
Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
50 55 60
gac tac att gac ttc ctg cag aga gtc ago ccc acc aat atg caa ggc 240
Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65 70 75 80
ttc acc aag agt ctt aat gcc ttc aac gta ggc gat gac tgc cca gtg 288
Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
85 90 95
ttt ccc ggg ctc ttt gag ttc tgc tgc cgt tac aca ggc gca tct ctg 336
Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
100 105 110
caa gga gca acc cag ctg aac aac aag atc tgt gat att gcc att aac 384
Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
115 120 125
tgg gct ggt ggt ctg cac cat gcc aag aag ttt gag gcc tct ggc ttc 432
Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe
130 135 140
tgc tat gtc aac gac att gtg att ggc atc ctg gag ctg ctc aag tac 480
Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
145 150 155 160

09598

cac cct cgg gtg ctc tac att gac att gac atc cac cat ggt gac ggg His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly 165 170 175	528
gtt caa gaa gct ttc tac ctc act gac cgg gtc atg acg gtg tcc ttc Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe 180 185 190	576
ctt aaa tac gga aat tac ttc ttc cct ggc aca ggt gac atg tat gaa Leu Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu 195 200 205	624
gtc ggg gca gag agt ggc cgc tac tac tgt ctg aac gtg ccc ctg cgg Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg 210 215 220	672
gat ggc att gat gac cag agt tac aag cac ctt ttc cag ccg gtt atc Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile 225 230 235 240	720
aac cag gta gtg gac ttc tac caa ccc acg tgc att gtg ctc cag tgt Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys 245 250 255	768
gga gct gac tot ctg ggc tgt gat cga ttg ggc tgc ttt aac ctc agc Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser 260 265 270	816
atc cga ggg cat ggg gaa tgc gtt gaa tat gtc aag agc ttc aat atc Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile 275 280 285	864
cct cta ctc gtg ctg ggt ggt ggt ggt tat act gtc cga aat gtt gcc Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala 290 295 300	912
cgc tgc tgg aca tat gag aca tog ctg ctg gta gaa gag gcc att agt Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser 305 310 315 320	960
gag gag ctt ccc tat agt gaa tac ttc gag tac ttt gcc cca gac ttc Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe 325 330 335	1008
aca ctt cat cca gat gtc agc acc cgc atc gag aat cag aac tca cgc Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg 340 345 350	1056
cag tat ctg gac cag atc ctc cag aca atc ttt gaa aac ctg aag atg Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met 355 360 365	1104
ctg aac cat gca cct agt gtc cag att cat gac gtg cct gca gac ctc Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu 370 375 380	1152
ctg acc tat gac agg act gat gag gct gat gca gag gag agg ggt cct Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro 385 390 395 400	1200
gag gag aac tat agc agg cca gag gca ccc aat gag ttc tat gat gga Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly 405 410 415	1248
gac cat gac aat gac aag gaa agc gat gtg gag att taa Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile 420 425	1287

<210> 20
 <211> 428
 <212> PRT
 <213> Artificial

<220>

09598

<223> Dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3)
gene

<400> 20

Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
1 5 10 15

His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
20 25 30

His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
35 40 45

Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
50 55 60

Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65 70 75 80

Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
85 90 95

Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
100 105 110

Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
115 120 125

Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe
130 135 140

Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
145 150 155 160

His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
165 170 175

Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
180 185 190

Leu Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu
195 200 205

Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg
210 215 220

Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile
225 230 235 240

Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys
245 250 255

Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser
260 265 270

Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile
275 280 285

09598

Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala
290 295 300

Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser
305 310 315 320

Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe
325 330 335

Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg
340 345 350

Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met
355 360 365

Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu
370 375 380

Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro
385 390 395 400

Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly
405 410 415

Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile
420 425

<210> 21
<211> 1458
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1458)
<223> human N-CoR (RD3) gene

<400> 21
gaa gtc ott cag cct gct cca cat caa gtg ata act aat ctc cct gaa 48
Glu Val Leu Gln Pro Ala Pro His Gln Val Ile Thr Asn Leu Pro Glu
1 5 10 15
ggc gtt cgg ott cgg aca act cga cca acc agg cca cgg ccc cct ctc 96
Gly Val Arg Leu Pro Thr Thr Arg Pro Thr Arg Pro Pro Pro Pro Leu
20 25 30
atc ccg tca tcc aaa acc aca gtg gct tca gaa aaa cca tct ttt ata 144
Ile Pro Ser Ser Lys Thr Thr Val Ala Ser Glu Lys Pro Ser Phe Ile
35 40 45
atg gga ggc tcc atc tca cag gga aca cca ggc act tat ttg act tct 192
Met Gly Gly Ser Ile Ser Gln Gly Thr Pro Gly Thr Tyr Leu Thr Ser
50 55 60
cat aat cag gct tcc tac act caa gaa aca ccc aag ccg tca gta gga 240
His Asn Gln Ala Ser Tyr Thr Gln Glu Thr Pro Lys Pro Ser Val Gly
65 70 75 80
tct atc tct ott gga ctg cca cgg caa cag gaa tct gcc aaa tca gct 288
Ser Ile Ser Leu Gly Leu Pro Arg Gln Gln Glu Ser Ala Lys Ser Ala
85 90 95
act ttg ccc tac atc aag cag gaa gaa ttt tct ccc cga agc caa aac 336
Thr Leu Pro Tyr Ile Lys Gln Glu Glu Phe Ser Pro Arg Ser Gln Asn
100 105 110

(44)

tca caa cct gag ggt ctg ttg gtc agg gcc caa cat gaa ggt gta gtc Ser Gln Pro Glu Gly Leu Leu Val Arg Ala Gln His Glu Gly Val Val 115 120 125	384
aga ggt acc gca gga gcc ata caa gaa gga agt ata act cgg gga act Arg Gly Thr Ala Gly Ala Ile Gln Glu Gly Ser Ile Thr Arg Gly Thr 130 135 140	432
cca acc agc aaa att tca gtg gag agc att cca tcc cta cgg ggc tct Pro Thr Ser Lys Ile Ser Val Glu Ser Ile Pro Ser Leu Arg Gly Ser 145 150 155 160	480
atc act cag ggc acc ccg gct ctg ccc cag act ggc ata cca aca gag Ile Thr Gln Gly Thr Pro Ala Leu Pro Gln Thr Gly Ile Pro Thr Glu 165 170 175	528
gct ttg gtg aag ggg tcc att tcg aga atg ccc att gaa gac agc agt Ala Leu Val Lys Gly Ser Ile Ser Arg Met Pro Ile Glu Asp Ser Ser 180 185 190	576
cct gag aaa ggc aga gag gaa gct gca tcc aaa ggc cat gtt att tat Pro Glu Lys Gly Arg Glu Glu Ala Ala Ser Lys Gly His Val Ile Tyr 195 200 205	624
gaa ggc aaa agt gga cat atc ttg tca tat gat aat att aag aat gcc Glu Gly Lys Ser Gly His Ile Leu Ser Tyr Asp Asn Ile Lys Asn Ala 210 215 220	672
cga gaa ggg act agg agt cca aga aca gct cat gaa atc agt tta aag Arg Glu Gly Thr Arg Ser Pro Arg Thr Ala His Glu Ile Ser Leu Lys 225 230 235 240	720
aga agc tat gaa tca gtg gaa gga aat ata aag caa ggg atg tca atg Arg Ser Tyr Glu Ser Val Glu Gly Asn Ile Lys Gln Gly Met Ser Met 245 250 255	768
agg gag tct cct gta tca gca ccg tta gag ggg ctg ata tgc cga gca Arg Glu Ser Pro Val Ser Ala Pro Leu Glu Gly Leu Ile Cys Arg Ala 260 265 270	816
tta ccc agg ggg agt cct cat tct gac ctc aaa gaa agg act gta ttg Leu Pro Arg Gly Ser Pro His Ser Asp Leu Lys Glu Arg Thr Val Leu 275 280 285	864
tct ggc tcc ata atg cag ggg aca cca aga gca aca act gaa agc ttt Ser Gly Ser Ile Met Gln Gly Thr Pro Arg Ala Thr Thr Glu Ser Phe 290 295 300	912
gaa gat ggc ctt aaa tat ccc aaa caa att aaa agg gaa agt cct ccc Glu Asp Gly Leu Lys Tyr Pro Lys Gln Ile Lys Arg Glu Ser Pro Pro 305 310 315 320	960
ata cga gca ttt gaa ggt gcc att acc aaa gga aaa cca tat gat ggc Ile Arg Ala Phe Glu Gly Ala Ile Thr Lys Gly Lys Pro Tyr Asp Gly 325 330 335	1008
atc acc acc atc aaa gaa atg ggg cgt tcc att cat gag att cca agg Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile Pro Arg 340 345 350	1056
caa gat att tta act cag gaa agt cgg aaa act cca gaa gtg gtc cag Gln Asp Ile Leu Thr Gln Glu Ser Arg Lys Thr Pro Glu Val Val Gln 355 360 365	1104
agc aca cgg ccg ata att gag ggt tcc att tcc cag ggc aca cca ata Ser Thr Arg Pro Ile Ile Glu Gly Ser Ile Ser Gln Gly Thr Pro Ile 370 375 380	1152
aag ttt gac aac aac tca ggt caa tct gcc atc aaa cac aat gtc aaa Lys Phe Asp Asn Asn Ser Gly Gln Ser Ala Ile Lys His Asn Val Lys 385 390 395 400	1200
tcc tta atc acg ggg cct agc aaa cta tcc cgt gga atg cct ccg ctg Ser Leu Ile Thr Gly Pro Ser Lys Leu Ser Arg Gly Met Pro Pro Leu	1248

09598

405

410

415

gaa att gtg cca gag aac ata aaa gtg gta gaa cgg gga aaa tat gag 1296
 Glu Ile Val Pro Glu Asn Ile Lys Val Val Glu Arg Gly Lys Tyr Glu
 420 425 430

gat gtg aaa gca ggc gag acc gtg cgt tcc cgg cac acg tca gtg gta 1344
 Asp Val Lys Ala Gly Glu Thr Val Arg Ser Arg His Thr Ser Val Val
 435 440 445

agc tct ggc ccc tcc gtt ctt agg tcc aca ctg cat gaa gct ccc aaa 1392
 Ser Ser Gly Pro Ser Val Leu Arg Ser Thr Leu His Glu Ala Pro Lys
 450 455 460

gca caa ctg agc cct ggg att tat gat gac acc agt gca cgg agg acc 1440
 Ala Gln Leu Ser Pro Gly Ile Tyr Asp Asp Thr Ser Ala Arg Arg Thr
 465 470 475 480

cct gtg agt tat caa aac 1458
 Pro Val Ser Tyr Gln Asn
 485

<210> 22
 <211> 486
 <212> PRT
 <213> Homo sapiens

<400> 22
 Glu Val Leu Gln Pro Ala Pro His Gln Val Ile Thr Asn Leu Pro Glu
 1 5 10 15

Gly Val Arg Leu Pro Thr Thr Arg Pro Thr Arg Pro Pro Pro Pro Leu
 20 25 30

Ile Pro Ser Ser Lys Thr Thr Val Ala Ser Glu Lys Pro Ser Phe Ile
 35 40 45

Met Gly Gly Ser Ile Ser Gln Gly Thr Pro Gly Thr Tyr Leu Thr Ser
 50 55 60

His Asn Gln Ala Ser Tyr Thr Gln Glu Thr Pro Lys Pro Ser Val Gly
 65 70 75 80

Ser Ile Ser Leu Gly Leu Pro Arg Gln Gln Glu Ser Ala Lys Ser Ala
 85 90 95

Thr Leu Pro Tyr Ile Lys Gln Glu Glu Phe Ser Pro Arg Ser Gln Asn
 100 105 110

Ser Gln Pro Glu Gly Leu Leu Val Arg Ala Gln His Glu Gly Val Val
 115 120 125

Arg Gly Thr Ala Gly Ala Ile Gln Glu Gly Ser Ile Thr Arg Gly Thr
 130 135 140

Pro Thr Ser Lys Ile Ser Val Glu Ser Ile Pro Ser Leu Arg Gly Ser
 145 150 155 160

Ile Thr Gln Gly Thr Pro Ala Leu Pro Gln Thr Gly Ile Pro Thr Glu
 165 170 175

Ala Leu Val Lys Gly Ser Ile Ser Arg Met Pro Ile Glu Asp Ser Ser
 180 185 190

(46)

09598

Pro Glu Lys Gly Arg Glu Glu Ala Ala Ser Lys Gly His Val Ile Tyr
195 200 205

Glu Gly Lys Ser Gly His Ile Leu Ser Tyr Asp Asn Ile Lys Asn Ala
210 215 220

Arg Glu Gly Thr Arg Ser Pro Arg Thr Ala His Glu Ile Ser Leu Lys
225 230 235 240

Arg Ser Tyr Glu Ser Val Glu Gly Asn Ile Lys Gln Gly Met Ser Met
245 250 255

Arg Glu Ser Pro Val Ser Ala Pro Leu Glu Gly Leu Ile Cys Arg Ala
260 265 270

Leu Pro Arg Gly Ser Pro His Ser Asp Leu Lys Glu Arg Thr Val Leu
275 280 285

Ser Gly Ser Ile Met Gln Gly Thr Pro Arg Ala Thr Thr Glu Ser Phe
290 295 300

Glu Asp Gly Leu Lys Tyr Pro Lys Gln Ile Lys Arg Glu Ser Pro Pro
305 310 315 320

Ile Arg Ala Phe Glu Gly Ala Ile Thr Lys Gly Lys Pro Tyr Asp Gly
325 330 335

Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile Pro Arg
340 345 350

Gln Asp Ile Leu Thr Gln Glu Ser Arg Lys Thr Pro Glu Val Val Gln
355 360 365

Ser Thr Arg Pro Ile Ile Glu Gly Ser Ile Ser Gln Gly Thr Pro Ile
370 375 380

Lys Phe Asp Asn Asn Ser Gly Gln Ser Ala Ile Lys His Asn Val Lys
385 390 395 400

Ser Leu Ile Thr Gly Pro Ser Lys Leu Ser Arg Gly Met Pro Pro Leu
405 410 415

Glu Ile Val Pro Glu Asn Ile Lys Val Val Glu Arg Gly Lys Tyr Glu
420 425 430

Asp Val Lys Ala Gly Glu Thr Val Arg Ser Arg His Thr Ser Val Val
435 440 445

Ser Ser Gly Pro Ser Val Leu Arg Ser Thr Leu His Glu Ala Pro Lys
450 455 460

Ala Gln Leu Ser Pro Gly Ile Tyr Asp Asp Thr Ser Ala Arg Arg Thr
465 470 475 480

Pro Val Ser Tyr Gln Asn

<210> 23
 <211> 731
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(731)
 <223> 5'-flanking region of Human interleukin-2 (IL-2) gene

<400> 23
 ctgagtattt aacaatcgca ccctttaaaa aatgtacaat agacattaag agacttaaac 60
 agatatataa tcatttttaa ttaaaatagc gttaaacagt acctcaagct caataagcat 120
 ttttaagtatt ctaatcttag tatttctcta gctgacatgt aagaagcaat ctatcttatt 180
 gtatgcaatt agctcattgt gtggataaaa aggtaaaacc attctgaaac aggaaaccaa 240
 tacacttctt gtttaatcaa caaatctaaa catttattct tttcatctgt ttactcttgc 300
 tcttgtccac cacaatatgc tattcacatg ttcagtgtag ttttaggaca aagaaaattt 360
 tctgagttac ttttztatcc ccacccctt aaagaaagga ggaaaaactg tttcatcacag 420
 aaggcgtaa ttgcataat tagagctatc acctaatgtt gggctaattg aacaagagg 480
 gatttcacct acatccattc agtcagttt tgggggttta aagaaattcc aaagagtcac 540
 cagaagagga aaaatgaagg taatgtttt tcagacaggt aaagtctttg aaaatatgtg 600
 taatatgtaa aacattttga ccccccata atatttttcc agaattaaca gtataaattg 660
 catctcttgt tcaagagttc cctatcactc tctttaatca ctactcacag taacctcaac 720
 tcttgccaca a 731

<210> 24
 <211> 527
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (73)..(506)
 <223> 5'-flanking region of Human interleukin-2 (IL-2) gene

<400> 24
 gggnnnnnng gngatctct accactatag ggcgaattga atttagcggc cgcganttog 60
 cccttgccta gctgctcttg tccaccacaa tatgctattc acatgttcag tgtagtttta 120
 ggacaaagaa aattttctga gttacttttg tatccccacc cccttaaaga aaggaggaaa 180
 aactgtttca tacagaaggc gtttaattga tgaattagag ctatcaccta agtgtgggct 240
 aatgtaacaa agagggattt cacctacatc cattcagtcg gtctttgggg gtttaaagaa 300
 attccaaaga gtcacagaa gaggaaaaat gaaggaatg tttttcaga caggtaaagt 360
 ctttgaaaat atgtgtaata tgtaaaacat ttgacaccc ccataatatt ttccagaat 420
 taacagtata aattgcatct cttgttcaag agttccctat cactctcttt aatcactact 480
 cacagtaacc tcaactctg ccacaagctt cgaaggcgga attcgtt 527

<210> 25
 <211> 900
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (57)..(875)
 <223> Promoter region of Human GATA-1 gene

<400> 25
 tgcctcttta ctatagggcg aattgaattt agcggccgcg aattcgccct tgatctatcc 60
 ctggctccca cctcagtttc ccgcctccaa ggcagcatgg cgggcaagaa gttgaggcca 120
 ctgtccctgg gtgttcctac cccacacccc tcacccaag acagcctgtt actgcggcgc 180
 caacagccac ggtgcctac atctgataag acttatctgc tgccccaggg caggccggag 240
 ctggcgtaag cccagtggtg gcgctaagtg agtgtgcccc tgcctccgcg cagcactggc 300
 ctggcctgca ggcttagcct gggtcacaa ggtatccac aggccttagt tcaaattccag 360
 cagaacctct ctgagcctca ctcttctcac ctgcaaaatg ggtacagcca catcccttct 420
 ctccctgcag ccaggaagac gcacatacac aggagtctag cccacaccgg ccccgacaaa 480
 attaagggtt ttactctctg aaaagcccag tgaagtcacg aaaccatata tgctattttc 540
 atttatcttg gtttcagcct attttgcttg tctggacact acagtccacg ggagcctagg 600
 tcgagcgagg tccaagaatc cccagggtgg gcaggagggg tggaagaggg cctccagtgc 660
 ccaagagggtg cccacacaagc atgggacccc cccctcccc tggactgccc caccactgg 720
 ggcaccagcc actccctggg gaggaggag gagggagaag ggaggagggg agggaggag 780
 gaaggagcc tcaaaggcca aggccagcca ggacaccccc tgggatcaca ctgagcttgc 840
 cacatcccca aggcggccga accctccgca accaccaaag cttataaggg cgaattcgtt 900

<210> 26
 <211> 660
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (11)..(647)
 <223> Promoter region of Human GATA-1 gene

<400> 26
 ttatggtacc accccagaag atgccaggag ggagttagcc agtcaggga ggcttccgag 60
 aagagaggac attgaagaag agtctcaaac ttaggcctga cggagaagac gcgcggccag 120
 gacacccac cccgcctc gtctcccca aagcctgac tggccccact gattccctta 180
 tctgccact ccagctgcc tccttgctgg ctgaactgtc gccgcagact tctgagcctg 240
 cgccccctcc acggggatgg gggagggaat ggggtgaggc ctggcctcac agcctcggg 300
 ttccagctc ttgctggagg cagggtctg gggcgcccta ctctcacc ttggcttctc 360
 ttctgagcg ctctgtgctc tccagaaatg aagaaatggg gtgagtcag cggccaaacc 420
 cttgttttag ctcttagaca tgcctcgagc ctgccattcc ctgtgaggac agatttccct 480
 atgttgcgac cgctgcttct aataataata atgatgatga taattccat ttacagagca 540
 caccatttat ggtgtgccag caggccctgt gctgagtgtt tcctaccac gtggggggct 600
 aggactttac ccgttttcca gatgaagaaa ctgaggctca gaggcgcta gcataagggc 660

<210> 27
 <211> 32
 <212> DNA

<213> Artificial

<220>

<223> PCR primer for amplifying the 5'-flanking region of Human interleukin-2 (IL-2) gene

<400> 27
tcgctagcct gagtatttaa caatgcacc ct 32

<210> 28
<211> 30
<212> DNA
<213> Artificial

<220>

<223> PCR primer for amplifying the 5'-flanking region of Human interleukin-2 (IL-2) gene

<400> 28
cgaagcttgt ggcaggagtt gaggttactg 30

<210> 29
<211> 777
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(777)

<223> Corresponding to the sequence (+661 to +1437) in the GenBank database (Accession: HSIL05)

<400> 29
atcagtatcc ttgaatcgaa acctttttct gagtatttaa caatgcacc ctttaaaaaa 60
tgtacataga cattaagaga cttaaacaga tatataatca ttttaaatta aaatagcgtt 120
aaacagtacc tcaagctcaa taagcatttt aagtattcta atottagtat ttctotagct 180
gacatgtaag aagcaatcta tottattgta tgcaattagc totttgtgtg gataaaaagg 240
taaaaccatt ctgaaacagg aaaccaatac acttctgtt taatcaacaa atctaaacat 300
ttattctttt catctgttta ctcttgcctc tgcaccac aatatgctat tcacatgttc 360
agtgtagttt tatgacaaag aaaattttct gaggtaacttt tgtatcccca ccccttaaa 420
gaaaggagga aaaactgttt catacagaag gcgttaattg catgaattag agctatcacc 480
taagtgtggg ctaatgtaac aaagagggat ttcacctaca tccattcagt cagtotttgg 540
gggtttaaag aaattccaaa gagtcatcag aagaggaaaa atgaaggtaa tgttttttca 600
gactggtaaa gtctttgaaa atatgtgtaa tatgtaaac attttgacac ccccataata 660
ttttccaga attaacagta taaattgcat ctcttgttca agagttccct atcactcttt 720
aatcactact cacagtaacc tcaactcctg ccacaatgta caggatgcaa ctctctgt 777

<210> 30
<211> 30
<212> DNA
<213> Artificial

<220>

<223> PCR primer for amplifying the 5'-flanking region of Human interleukin-2 (IL-2) gene

<400> 30
cgctagctgc tcttgtccac cacaatatgc 30

<210> 31
 <211> 538
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(538)
 <223> Corresponding to the sequence (+901 to +1438) in the GenBank database
 (Accession: HSIL05)

<400> 31
 taaaaccatt ctgaaacagg aaaccaatac acttcctgtt taatcaacaa atctaaacat 60
 ttattctttt catctgttta ctcttgctct tgtccaccac aatatgtat tcacatgttc 120
 agtgtagttt tatgacaaag aaaattttct gagttacttt tgtatcccca ccccttaaa 180
 gaaaggagga aaaactgttt catacagaag gcgttaattg catgaattag agctatcacc 240
 taagtgtggg ctaatgtaac aaagagggat ttcacctaca tccattcagt cagtcttigg 300
 gggtttaag aaattccaaa gagtcatcag aagaggaaaa atgaaggtaa tgttttttca 360
 gactggtaaa gtctttgaaa atatgtgtaa tatgtaaaac attttgacac ccccataata 420
 tttttcaga attaacagta taaattgcat ctcttgttca agagttccct atcactcttt 480
 aatcactact cacagtaacc tcaactcctg ccacaatgta caggatgcaa ctctgtgc 538

<210> 32
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying the promoter region of Human GATA-1 gene

<400> 32
 atagatctat ccctggctcc cacctcag 28

<210> 33
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying the promoter region of Human GATA-1 gene

<400> 33
 ataagctttg gtggttgccg agggttcg 28

<210> 34
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying the promoter region of Human GATA-1 gene

<400> 34
 atggtaccac ccagaagat gccaggag 28

<210> 35
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying the promoter region of Human GATA-1 gene

<400> 35
 atgctagcgc cctctgagcc tcagtttc 28

<210> 36
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying a human histone deacetylase-1 (HDAC1) gene

<400> 36
 gaggaattca agatggcgca gac 23

<210> 37
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying a human histone deacetylase-1 (HDAC1) gene

<400> 37
 ggagcggccg cttcaggcca acttg 25

<210> 38
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying a human histone deacetylase-2 (HDAC2) gene

<400> 38
 ggggatccat ggcgtacagt caag 24

<210> 39
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying a human histone deacetylase-2 (HDAC2) gene

<400> 39
 ggtcggccg ccaaattcag gggttgctg 29

<210> 40
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying a human histone deacetylase-3 (HDAC3) gene

<400> 40
 ccggatccac catggccaag ac 22

<210> 41
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying a human histone deacetylase-3 (HDAC3) gene

<400> 41
 gcagcggccg ccactotta atctccac 28

<210> 42
 <211> 28
 <212> DNA
 <213> Artificial

<220>

<223> PCR primer for amplifying a human histone deacetylase-4 (HDAC4) gene

<400> 42
 gggaattcat gagctcccaa agccatcc 28

<210> 43
 <211> 29
 <212> DNA
 <213> Artificial

<220>

<223> PCR primer for amplifying a human histone deacetylase-4 (HDAC4) gene

<400> 43
 aaggcgccgc agcttcgagg gagtgtctac 29

<210> 44
 <211> 27
 <212> DNA
 <213> Artificial

<220>

<223> PCR primer for amplifying a human histone deacetylase-5 (HDAC5) gene

<400> 44
 ggcaagctta tgaactctcc caacgag 27

<210> 45
 <211> 29
 <212> DNA
 <213> Artificial

<220>

<223> PCR primer for amplifying a human histone deacetylase-5 (HDAC5) gene

<400> 45
 gggcgccgc gtcacagggc aggctcctg 29

<210> 46
 <211> 27
 <212> DNA
 <213> Artificial

<220>

<223> PCR primer for amplifying a human histone deacetylase-6 (HDAC6) gene

<400> 46
 gcgaagctta tgacctcaac oggccag 27

<210> 47
 <211> 33
 <212> DNA
 <213> Artificial

<220>

<223> PCR primer for amplifying a human histone deacetylase-6 (HDAC6) gene

<400> 47
 gcatgcggcc gcttagtgtg ggtggggcat atc 33

<210> 48

<211> 26
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying a human histone deacetylase-7 (HDAC7) gene

<400> 48
 cgaattcagc cgcagcccat ggacct 26

<210> 49
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying a human histone deacetylase-7 (HDAC7) gene

<400> 49
 cggtagccctg tgcaccogga tcacgg 26

<210> 50
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying a human histone deacetylase-8 (HDAC8) gene

<400> 50
 cgaattcttt aagcggaaga tggagg 26

<210> 51
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying a human histone deacetylase-8 (HDAC8) gene

<400> 51
 aggtaccgac cacatgcttc agattc 26

<210> 52
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying a human histone deacetylase-3 (HDAC3) gene

<400> 52
 ctgaattcac catggccaag accg 24

<210> 53
 <211> 61
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for adding a Flag sequence to a human histone deacetylase-3 (HDAC3) gene

<400> 53
 gggcggccgc ctacttgta togtcgtcct tgtaatcgg accaatctcc acatogcttt 60

c 61

<210> 54

<211> 8
 <212> PRT
 <213> Artificial

<220>
 <223> Flag sequence

<400> 54
 Asp Tyr Lys Asp Asp Asp Lys
 1 5

<210> 55
 <211> 31
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for adding a Kpn I site to a human histone deacetylase-1 (HDAC1) gene

<400> 55
 atcgggtaccg gccaaacttga cctcctcctt g 31

<210> 56
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for adding a Kpn I site to a human histone deacetylase-2 (HDAC2) gene

<400> 56
 atcgggtaccg gggttgctga gctgtttctg 29

<210> 57
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for adding a Bgl II site to a human histone deacetylase-4 (HDAC4) gene

<400> 57
 gatagatctc agggggcggt cctcttc 27

<210> 58
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <223> Nucleotide sequence having a Flag nucleotide sequence

<400> 58
 aattcctgca gagatctgat tacaaggacg acgatgacaa gtaggc 46

<210> 59
 <211> 46
 <212> DNA
 <213> Artificial

<220>
 <223> Nucleotide sequence having a Flag nucleotide sequence

<400> 59
 ggccgcctac ttgtcatcgt cgtccttgta atcagatctc tgcagg 46

<210> 60
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

<400> 60
 cagtgcaccc atatggaacg agg 23

<210> 61
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

<400> 61
 gcaagctttc caggggggcg 20

<210> 62
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

<400> 62
 cccccctggaa agcttgcgga 20

<210> 63
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

<400> 63
 gacatgtaca ggacgctagg gt 22

<210> 64
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H863L) of human histone deacetylase-4 (HDAC4) gene

<400> 64
 octgtacatg tccctccttc g 21

<210> 65
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H863L) of human histone deacetylase-4 (HDAC4) gene

<400> 65

atagatctag acaggggcgg

20

<210> 66
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 66
 gaggaattca agatggcgca gac

23

<210> 67
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 67
 ctgggacttc ttgcaagct tcagg

25

<210> 68
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 68
 gggcctgaag cttgcaaaga agtc

24

<210> 69
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 69
 gtgaatatca atgcaatgt acagc

25

<210> 70
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 70
 gacggcgtgg aagaggcctt c

21

<210> 71
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H199L) of human

histone deacetylase-1 (HDAC1) gene

<400> 71
gaagtactct ccatacttaa gaaagg 26

<210> 72
<211> 26
<212> DNA
<213> Artificial

<220>
<223> PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 72
ctgtgtcctt tottaagtat ggagag 26

<210> 73
<211> 22
<212> DNA
<213> Artificial

<220>
<223> PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 73
tctcggagcg ggtagttaac ag 22

<210> 74
<211> 23
<212> DNA
<213> Artificial

<220>
<223> PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 74
aaccagctg aacaacaaga tctg 23

<210> 75
<211> 26
<212> DNA
<213> Artificial

<220>
<223> PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 75
ctcaaacttc ttggcaagct tcagac 26

<210> 76
<211> 25
<212> DNA
<213> Artificial

<220>
<223> PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 76
tggtggtctg aagcttgcca agaag 25

<210> 77
<211> 21
<212> DNA
<213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 77
 cccgtcacca tggtaggatgt c 21

<210> 78
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3) gene

<400> 78
 tgacattgac atccaccatg gtg 23

<210> 79
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3) gene

<400> 79
 gaagtaattt ccgtacttaa ggaagg 26

<210> 80
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3) gene

<400> 80
 tgtccttcct taagtacgga aattac 26

<210> 81
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for creating a dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3) gene

<400> 81
 ggcacaaatg cagtgagggtt gg 22

<210> 82
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> PCR primer for amplifying RD3 sequence of human N-CoR gene

<400> 82
 gggtccgtg aagtccttca gcctgctcc 29

<210> 83
 <211> 29

<212> DNA
<213> Artificial

<220>

<223> PCR primer for amplifying RD3 sequence of human N-CoR gene

<400> 83

tgccggccgcc atgggtgagc ctctggaca

29

<210> 84

<211> 960

<212> DNA

<213> homo sapiens

<220>

<221> misc_feature

<222> (1)..(960)

<223> Corresponding to the sequence (+5281 to +6240) in the GenBank database
(Accession: AF196971)

<400> 84

```
gcctctgtct ctccactcc acccctttcc ttctctaccc tatccactc ctgaggaat      60
catccctggc tcccactca gtttcccgcc tocaaggcag catggcgggc aagaagtga      120
ggccactgtc cctgggtgtt cctaccccca caccctcacc ccaagacago ctgttactgc      180
ggcgccaaca gccacggtcg cctacatctg ataagactta tctgtgccc cagggcaggc      240
cggagctggc gtaagcccca gtggggcgct aagtgagtgt gccctgcct cccgccagca      300
ctggcctggc ctgcaggctt agcctgggtc atcaaggtat cccacaggct ctagtcaaa      360
tccagcagaa cctctctgag cctcactott ctccactgca aaatgggtac agccacatcc      420
cttctctccc tgcagccagg aagacgcaca tacacaggag tctagccac accggccccg      480
cacaaattaa gggctttact ctctgaaaag ccagtgaaag tcatgaaacc atatctgcta      540
ttttcattta tcttggtttc agcctatitt gcttgtctgg aactacagt ccacgggagc      600
ctaggtcgag cgaggctcaa gaatccccag ggtgggcagg gaggtggaa gagggcctcc      660
agtgcccaag aggtgcccc caagcatggg acccgcccc tccctggac tgccccaccc      720
actggggcac cagccactcc ctggggagga gggaggagg agaaggagg gagggaggga      780
gggagggaagg gagcctcaaa ggccaaggcc agccaggaca cccctggga tcacactgag      840
cttgccacat cccaaggcg gccgaacct ccgcaaccac cagccagggt cagtctcagc      900
cccagagag cccccaccaa ggcaaccctg ggctgtctgc cctaccctt atgcttgctc      960
```

<210> 85

<211> 720

<212> DNA

<213> homo sapiens

<220>

<221> misc_feature

<222> (1)..(720)

<223> Corresponding to the sequence (+2321 to +3040) in the GenBank database
(Accession: AF196971)

<400> 85

```
gtacaaatgc catgggcct ggaccaagca ggggtctag aaccccagaa gatgccagga      60
gggagtgagc cagtccagga aggtctccga gaagagagga cattgaagaa gagtctcaaa      120
cttaggcctg acggagaaga cgcggggcca ggacacccca ccccgccct cgtctcccc      180
aaagcctgat ctggccccac tgattccctt atctgcccc tccagctgc ctcccttgctg      240
```

09598

gctgaactgt cgccgcagac ttctgagcct gcgccccctc cacggggatg ggggagggaa	300
tggggtgagg cctggcctca cagcctcggg gtttcagct cttgctggag gcagggctct	360
ggggcgccct actcctcacc cttggcttct ctctctgagc gctctgtgct ctccagaaat	420
gaagaaatgg ggtgagtcca gcggccaaac ctttgtotta gctcttagac atgcctcgag	480
cctgccatto cctgtgagga cagatttccc tatgttgca ccgctgcttc taataataat	540
aatgatgatg ataattccca tttacagagc acaccattta tgggtgtcca gcaggccctg	600
tgctgagtgg ttctaccca cgtggggggc taggacttta cccgttttcc agatgaagaa	660
actgaggctc agagggcgtc tggcccagga atcacacagc aaatcacaca gcaaatcaga	720

<210> 86
 <211> 12
 <212> DNA
 <213> homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(12)
 <223> Palindrome sequence found on the 3' side of the GATA-E-box motif in promoter region of human GATA-1 gene

<400> 86	
ctgtggccac ag	12

92/123